

OM of: US-09-805-550-4 to: EST:* out-format : pfs
Date: Aug 31, 2002 4:58 AM
About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL=frame+2pn.model -DEV=xlh
-O=/cgn2.1/USPTO_spool/US09805550/runat_29082002.160721.29030/app-query.fasta.1.897
-DB=EST -OFMT=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELLOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODEL=LOCAL -OUTFMT=pfs -NOR=ext -HEA=SIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09805550.ecgnl.1.3201
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIME=OUT=120 -WARN_TIME=OUT=30
-NO_XLPIXT -WAIT -THREADS=1

Search information block:

Query: US-09-805-550-4
Query length: 368
Database: EST*
Database sequences: 13736207
Database length: -1841457050
Search time (sec): 2392.770000

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
gb_est1:AV910230	+	894.50	1169.45	632	AV910230 AV910230 K. Sato unpubl
gb_est2:BE442895	+	788.50	1031.07	616	BE442895 WHB1107 A10.B192S Whea
gb_est2:BE366895	+	729.50	955.90	503	BE366895 HVSMH002010f Hordeum
gb_est2:BE360535	+	716.50	937.08	605	BE360535 DGL_64_F06.D1.A002 Dat
gb_est2:BE510592	+	704.00	924.64	407	BE510592 946054A04.y1 946 - ta
gb_est1:AV912395	+	652.00	850.33	414	B1927022 EST5456911 tomato flowe
gb_est2:BE510591	-	637.00	832.96	37	AV912395 AV912395 K. Sato unpubl
gb_est2:BE510591	-	633.00	832.85	36	BE510591 946054A04.xl 946 - ta
gb_est1:BI925179	+	628.00	819.07	22	BI925179 EST545068 tomato flowe
gb_est1:BE035647	+	628.50	814.75	36	BE035647 MO13A05 MO Mesembryant
gb_est1:AM508593	+	612.50	799.78	27	AM508593 s134a09.y1 Gm-cl050 G
gb_est2:BE445098	+	612.00	796.50	89	BE445098 GA_Pa0026M08f Gossyp
gb_est2:BE685286	+	604.50	787.64	13	BE685286 EST487049 MHAM Medicag
gb_est2:BI973998	+	602.50	788.20	59	BI973998 sa195d11.y1 Gm-cl065 G
gb_est2:BM113219	+	593.50	774.90	65	BM113219 EST560755 potato rootc
gb_est2:BE591983	+	590.50	770.79	70	BE591983 EST499825 P. Infestans
gb_est2:BE447033	+	587.00	763.74	90	BE447033 GA_EB0040E14f Gossyp
gb_est2:BE6450691	+	583.50	764.51	526	BE6450691 sad98c06.y1 Gm-cl055 G
gb_est2:BE453539	+	578.50	755.69	66	BE453539 NF093C03LFI1019 Devel
gb_est2:BE704885	+	568.50	740.55	81	BE704885 SC01_02c08.A SC01_AAR
gb_est2:BE604586	+	566.00	739.25	66	BE604586 saad07g06.y1 Gm-cl058 G
gb_est2:BE588991	+	565.00	736.17	93	BE588991 EST490800 MHRP-Medica
gb_est2:BE067283	+	564.50	737.95	62	BE067283 st37g08.y1 Gm-cl067 G
gb_hic:BC003846	+	564.00	732.06	11	BC003846 Mus musculus, Stimlat
gb_est2:BE585808	+	561.00	731.92	11	BE585808 Est42prt.E07.e7.051 KS
gb_est2:BE445328	+	557.00	725.60	81	BE445328 GA_Pa0027E22f Gossyp
gb_est2:BM271253	+	555.50	727.19	29	BM271253 sak07a10.y1 Gm-cl075 G
gb_est1:AT856811	+	553.00	724.79	40	AT856811 sb78e08.y1 Gm-cl010 G
gb_est1:AV932070	+	550.50	719.31	81	AV932070 AV932070 K. Sato unpubl
gb_est2:BE6351432	+	547.00	712.59	80	BE6351432 108805 Mature tuber 1a
gb_est2:BE645485	+	541.00	703.85	78	BE645485 GA_Pa0028M06f Gossyp
gb_est2:BE1935539	+	540.50	704.94	30	BE1935539 EST555428 tomato flowe
gb_est2:BE681659	+	540.00	703.81	77	BE681659 EST483334 GVN Medicag
gb_est2:BM085128	+	539.50	706.04	57	BM085128 sa132e10.y1 Gm-cl066 G
gb_est2:BE633959	+	538.50	702.97	53	BE633959 EST344022 potato stold
gb_est2:BE009008	+	536.50	701.39	80	BE009008 ss72b10.y1 Gm-cl062 G
gb_est2:BE647902	+	534.50	696.47	72	BE647902 EST509521 HOGA Medicag
gb_est1:AT1726909	+	533.50	698.19	57	AT1726909 BN1681621 Six-day G
gb_est2:BE686047	+	532.50	694.13	76	BE686047 EST487812 MHAM Medicag
gb_est1:AM442310	+	530.50	692.87	66	AM442310 EST311706 tomato fruit

gb_est2:BI750564 - 527.50 688.12 4.4e-29 724 | BI750564 Ta01_07c08.R Ta01_A
gb_est2:BE602523 + 527.00 687.32 4.9e-29 735 | BE602523 HVSMH009314f Hord
gb_est2:BE645488 + 525.50 684.42 7.1e-29 808 | BE645488 EST507107 KV3 Medic
gb_est2:BE582388 - 524.00 681.92 9.8e-29 854 | BE582388 EST484131 GVN Medic
gb_est1:AI901927 - 523.00 686.31 5.6e-29 479 | AI901927 618012E05.xl 618 -

seq_name: gb_est1:AV910230

seq_documentation_block:

LOCUS AV910230 632 bp mRNA linear EST 18-JAN-2002
DEFINITION AV910230 K. Sato unpublished cDNA library, cv. Akashinriki
vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
baak3m04 5', mRNA sequence.
ACCESSION AV910230.1 GI:18205972
VERSION AV910230.1
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
/ Triticeae; Hordeum.
1 (bases 1 to 632)

REFERENCE Sato, K., Saitoh, D. and Takeda, K.

AUTHORS Barley EST sequencing project in NIG and Okayama Univ

JOURNAL Unpublished (2002)

COMMENT Contact: Tadashi Shin-1

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp.

location/Qualifiers

1..632

/organism="Hordeum vulgare subsp. vulgare"

/cultivar="Akashinriki"

/db_xref="taxon:112509"

/clone_lib="K. Sato unpublished cDNA library, cv.

Akashinriki vegetative stage leaves"

/tissue_type="leaves"

/dev_stage="vegetative stage"

147 c 166 g 150 t 1 others

BASE COUNT 168 a 147 c 166 g 150 t 1 others

ORIGIN

alignment_scores:

Quality: 894.50 Length: 205

Ratio: 4.635 Gaps: 2

Percent Similarity: 94.146 Percent Identity: 84.878

alignment_block:

US-09-805-550-4 x AV910230 ..

Align seg 1/1 to: AV910230 from: 1 to: 632

161 AsplysAsplysValgIn.ArgAlaLeuArgAlaAlaTyrAsnAspProG 177

13 CATAGAGTAAAGTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 62

177 LuArgAlaValAlaGluTyrLeuTyrSerGlyIleProValThrAlaGluIle 193

63 AACGCGCATGACATCATCTGATCTGATCTGATCTGATCTGATCTGATCT 112

194 AlaValAlaProIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 210

113 GCTGTTGCGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 160

210 rGlyGlyAlaGlyLeuSerGlyIleProAsnThrAlaProLeuAspLeuP 227

161 GGAGAAACATGCGCTCTGAGATCCAAACACACACACACACACACACAC 209

227 heProGInGlyAlaSerAsnAlaGlyGlyGlyGlyGlyGlyGlyGlyGly 243

seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
210	TTCCCGAAGGGGCTTCCATGCTGAGGGTGCCTGCTGGTGGATCACTT	259												
244	ASPPheLeuArgHisAsnProGlnPheGlnAlaValArgGluMetValI	260												
260	GAATTTCTTCGAAATTAACCAACAGTTTCAAGCACTTCGGGAAATGGTCCA	309												
260	SPHrAsnProGlnIleLeuGlnProMetLeuValGluLeuSerIysGlnA	277												
310	TTCAAAATCCAAATTTTACAGCTATGCTCCAGAAATTGACCAACCA	359												
277	SNProGlnIleLeuArgLeuIleGluGlnAlaHisAspGluPheLeuGln	293												
360	ATCCCTCAACTTCTTAAGCTTGATTCAAGAGACAAATATATAGTTCCTTCA	409												
294	LeuLeuAsnGluProPheGlnGlyGlyGlyGlyAspPheLeuAspGlnP	310												
410	TTTACTAAATGAGACATTTGTAAGCGCGCATGGGACCTTCTTAGACCA	459												
310	oGluGluAspGluMetProHisAlaIleSerValThrProGluGluGln	327												
460	TGACCCAGATGATGAAATGCTCATGCTTCAAGTGAGACCAAGAACCA	509												
327	JulAlaIleGlyArgLeuGlnIleSerMetGlyPheAspArgAlaArgVal	343												
510	AGGCATTTGGAAAGTTTGAAGCCATGGGTTTGAGAGACAGCTGTCAAT	559												
344	GluAlaPheLeuAlaCysAspArgAsnGluLeuAlaAlaAsnTyrLe	360												
560	GAAGCATTTCTTCGCCCTGTGACAGAAATGAGCAATCGTCGCAAAATCAT	609												
360	uLeuGluHisAla	364												
610	TCTTGAGCATGCC	622												
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	source
seq_name: gb_est2:BE442895	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS</					

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/clone.lib="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/notes="Vector: lambda Uni-ZAP XR, excised phagemid
phuescript SK: Site.1: EcoRI; Site.2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and ceftaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give phuescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HP Nuyve
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)".
```

BASE COUNT 161 a 158 c 153 g 143 t 1 others

ORIGIN

Alignment_scores:

Quality:	788.50	Length:	206
Ratio:	4.239	Gaps:	3
Percent Similarity:	90.291	Percent Identity:	75.728

alignment_block:

US-09-805-550-4 x BE442895 ..

Align seg 1/1 to: BE442895 from: 1 to: 616

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39 TyrPrOTRPGLYGNGInleuLeuIIePhasngLYvsValleuLys 55
|||||
3 TATCCATGGGTCAACAACCTGCTGATTCACACAGCGCAAGGTTTGAAGA 52
|||||
55 pGluSerThrLeuGluGlnLysValLeuGluLysPheLeuVal 72
|||||
53 TGAAGCACATTGGATGAAATCAAGTTACGAAAGATGATTTCTGATTG 102
|||||
72 aMetLeuSerLysGlyLysThrSerGlySerThrGlyThrSerSer 88
|||||
103 TCATGCTTAGCAAGATGAAGCTTCTCTCCAGTGAGGACTCATCTGCG 152
|||||
89 GlnHisSerAsnThrProAlaThrArgGlnAlaProProLeuGlnAla 105
|||||
153 CAGCCCTTCACGACTCGTGTACCAAGTCAAGCACCTCCAGTGTCTCAACC 202
|||||
105 oGlnGlnAlaProGlnProProValAlaProIleThrThrSerGlnPro 122
|||||
203 A...CAAGCTCTCAGCCGCCAGGTCCCATCACTACGACTTCTCAGCCTG 249
|||||
122 IuGlyLeuProAlaGlnAlaPro...AsnThrHisAspAsnAlaLeuSer 137
|||||
250 AAAAGCACCCGCGAGAGACCCCTTCGATGACAGTTGATCTTGACAGCATG 299
|||||
138 AsnLeuLeuSerGlyArgAsnValAspThrIleIleAsnGlnLeuMet 154
|||||
300 GATTTACATGTCAGAGAACCAATCTGGACACATATATTAAACAGATATGGA 349
|||||
154 uMetGlyGlyLysSerThrPaspLysAspLysValGlnAlaGlnAlaLeuArg 171
|||||
350 GATGGGGGGGTGGCAGCTGGGACAGATTAAGTCCCAAGAGCTCTCCGGTG 399
|||||
171 IaAlaTyrAsnAsnProGluArgAlaValGluTyrLeuTyrSerGlyIle 187
|||||
400 CTGCTTATAACATCCAGAAAGGGCCATTGACATCTGTACTCTGTTATT 449
|||||
188 ProValThrAlaGluIleAlaValProIleGlyGlyGlnGlyAlaAsnTh 204
|||||
```

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450 CCAGTGCACGCTGAGGTTCCTGTTCCCGCGRGTTGGTCAAGGGGCAAAACAC 499

204 rThrsapargalAProthgLygluaAaglyteusergyllieProAsnt 221
||||| :|||::: |||||
500 CACTGATGCAGCTCCTCGNA...GAACCGGCCCTCTGTGAATCCCAAACA 546

221 hralAProteinuspheupheproIngLyAlaSerasnAaglyglycyl 237
||||| :|||::: |||||
547 CAGCACCATTAAGATCTTTCCACAGAGGGGCTTCATCTGTGAAGTGCT 596

238 ALaAgLyGLyProLeu 243
:::||||| ||
597 GTGGGGGTGCATCTT 614

seq_name: gb_est2.BG368695

seq_documentation_block:
LOCUS BG368695 503 bp mRNA linear EST 22-Oct-2001
DEFINITION HVSME10020E10f Hordeum vulgare 20 DAP spike EST library HVCDNA0010
(20 DAP) Hordeum vulgare cDNA clone HVSME10020E10f, mRNA sequence.
ACCESSION BG368695
VERSION BG368695.2 GI:16325408
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 503)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Fritsch,D., Yu
,Y., Henry,D., Palmer,M., Rambo,J., Simmons,J., Chol,D.W., Fenton
,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 20 DAP spike cDNA library
Unpublished (2001)
On Mar 8, 2001 this sequence version replaced gi:13257796.

JOURNAL
COMMENT Contact: Wing RA
Clemons University Genomics Institute
100 Jordan Hall, Clemons, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwinge@clemons.edu
Total hg bases = 475
Seq primer: AATTACCCTCCTACTTAAGG
High quality sequence stop: 503.
Location/Qualifiers
1..503
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSME10020E10f"
/clone_lib="Hordeum vulgare 20 DAP spike EST library
HVCDNA0010 (20 DAP)"
/libsize-type="20 DAP spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 20 DAP (Fenton
). Total RNA was prepared, poly(A) RNA was purified, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give plasmid SK(-) cDNA
phagemids in the TJ Close lab at the University of
California, Riverside (chol). Phagemids were plated and
picked at the Clemons University Genomics Institute (CUGIR)
(Begum, Palmer, Fritsch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Fritsch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
```

REFERENCE 1 Clade: Panicoidae; Andropogoneae; Sorghum.
1 (bases 1 to 605)
Cordonier-Pratt,M., Gingle,A., Marsala,C., Sudman,M. and Pratt
L.H.
An EST database from Sorghum: dark-grown seedlings
JOURNAL Unpublished (2000)
COMMENT Department: Cordonier-Pratt MM
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpatr@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 567
POLYA-No.

FEATURES
SOURCE Location/Qualifiers
1..605
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings. Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector Lambda Zap II.
Clones to be sequenced were prepared by mass excision."

BASE COUNT 166 a 178 c 152 g 109 t
ORIGIN

alignment_scores:
Quality: 716.50 Length: 152
Ratio: 4.841 Gaps: 1
Percent Similarity: 97.368 Percent Identity: 92.763

alignment_block:

US-09-805-550-4 x BE360535 ..
Align seg 1/1 to: BE360535 from: 1 to: 605

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1 Mettyleuethrvallysthrleuylsglythrhishpheglutleargva 17
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148 ATAAAGCTGACGGTGAAGACCCCTCAAGGGCAGCAGCTCGAGATCCGGGT 197
|||||
17 Tglnproasnspthrilemetalaavallyslyasnileglutleag 34
|||||
198 GCAGCCCAAGACACGATGTGGCTGTGAAGAGAACATCGAAGAGATAC 247
|||||
34 Tngilyllyaspsertyrproctrglycnglnleuleuilepheasnngly 50
|||||
248 AAGCAAGAGGACACTATCCATGTGGGGCAACACTGCTGATTTCAATGGC 297
|||||
51 Lysvalleuylaspgluserthrleugluasnlysalasnngluas 67
|||||
298 AAGGCTCTGAAGATGAAGATGATGAGATGAATGAATGAAGCAAGA 347
|||||
67 pgllypheleuvalvalmetleuerysglylysthrserglyserthrg 84
|||||
348 TGGGTTTCTAGTGTCTATGCTTAGTAAGGTAAACATCTGGTTCAGTGT 397
|||||
84 LyrthrserSerSerGlnHisSerAsnThrProalathrarGlnAlaPro 100
|||||
398 GAACCTTCATCTTCCAGCCCTCAACACCTCTGACAGCAAGGACGACCT 447
|||||
101 FrcleugluabaproGlnGlnAlaProGlnProProValAlaProIleth 117
|||||
448 CCGCTGATATGCCCAACAAGCTCCACACCCCGGTGACACCACTAC 497
|||||
117 rThrSerGlnProGluGlyLeuProAlaGlnAla...ProAsnThrHis 133
|||||
498 AACTTCTGAGCTGAAAGACTTCTGACAGGCTCCCTCTTAACACATATGT 547

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133 spasnalaaserasnleuenserGlyargasnvalasprhileile 149
|||||
548 ACAATGCAGCATCAATGCTTCTATCAGGAAGCAATGTGACACATATATT 597
150 AsnGln 151
|||||
598 AACCG 603

seq_name: gb_est2:BE510592

seq_documentation_block:
LOCUS BE510592 407 bp mRNA linear EST 07-AUG-2000
DEFINITION 946054A04.y1 946 - tassal primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION BE510592
VERSION BE510592.1 GI:9731840
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade: Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 407)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946054 row: A column: 04.

FEATURES
SOURCE Location/Qualifiers
1..407
/organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassal primordium prepared by Schmidt
lab"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="XLOLR"
/note="Organ: tassels. Vector: HybriZAP; Site_1: EcoRI;
Site_2: XhoI; George Chuck dissected immature tassels
between Imm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 kb with a 1 kb average."

BASE COUNT 134 a 91 c 95 g 87 t
ORIGIN

alignment_scores:
Quality: 704.00 Length: 135
Ratio: 5.215 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-805-550-4 x BE510592 ..
Align seg 1/1 to: BE510592 from: 1 to: 407

```

28 Lysasnileglutlileglnlyllyaspsertyrprotrpglyglnl 44
|||||
2 AAGAAATATTGAAGATGACAAAGGAAAGACACATCAACGAGGCGCCACA 51
|||||
44 nleuilelepheasnnglyllysalasnlyaspgluserthrleugln 61
|||||
52 ACTGCTGATTTCAATGGAAGGCTTGAAAGATGAAAGATGACATTTGAGAG 101

```

```

61  luasnlyrsValasngluaspolyphleuValaMetleuSerlysgly 77
    |||||||
102  AGAATAAGCAATGAGATGGGTTCTAGTGTGCTAGTAAGAGGT 151
    |||||||
78  LysThrsSerlySerThrsThrsSerSerSerInhisSerAsnThrPr 94
    |||||||
152  AAAACAATCTGTTCACTGCAACTTCACTTCCAGCAGCTCAAACTCC 201
    |||||||
94  oAlaThrsArgGlnAlaProLeuGlnAlaProGlnAlaProGln 111
    |||||||
202  TGCACACAGCAGCAGCCTCTCTAGAGGCCCAACACAGCTCTCAAC 251
    |||||||
111  roProValAlaProIleThrsThrsSerGlnProGlnlyLeuProAlaGln 127
    |||||||
252  CCCGGTGGCACAATTAACAATCTCTCAGCCTGAAGACTCTCTGACAG 301
    |||||||
128  AlaProAsnThrHisAspAsnAlaAlaSerAsnleuSerGlyArgAs 144
    |||||||
302  GCACCTTAACACACATGCAATGCGCATCAATCTCTGCTGGAAGGAA 351
    |||||||
144  nValAspThrIleIleAsnGlnleuMetGluMetGlyGlySerThrPA 161
    |||||||
352  TGTTCACACATATATTAACCACTAATGACATGGTGGGAGATTGGG 401
    |||||||
161  splyrs 162
    |||||
402  ACAA 406

```

seq_name: gb_est2:BI927022

seq_documentation_block:

LOCUS BI927022 771 bp mRNA linear EST 18-OCT-2001
 DEFINITION EST546911 tomato flower, 3 - 8 mm buds Lycopersicon esculentum cDNA
 clone cTOB21A11 5' end, mRNA sequence.

ACCESSION BI927022
 VERSION BI927022.1 GI:16236126

KEYWORDS EST.

SOURCE tomato.

ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

REFERENCE 1 (bases 1 to 771)
 van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,
 Uiterback,T., Van Aken,S., Ronning,C.M., Niemman,W., Fraser,C.M.,
 Martin,G.B., Giovannoni,J.D. and Tanksley,S.D.
 Generation of ESTs from tomato flower tissue, 3-8 mm buds (2001)

AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Unpublished (2001)
 Contact: CUGI
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 This clone is available through the Clemson University Genomics
 Institute

Seq primer: 73.

FEATURES
 source Location/Qualifiers

```

1..771
  /organism="Lycopersicon esculentum"
  /cultivar="TA496"
  /db_xref="taxon:4081"
  /clone="cTOB21A11"
  /clone_lib="tomato flower, 3 - 8 mm buds"
  /tissue_type="flower"
  /dev_stage="3-8mm buds"
  /note="Vector: pBluescript SK(-); site_1: EcoRI; site_2:
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research. Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

```

BASE COUNT 213 a 160 c 180 g 218 t
 ORIGIN

alignment_scores:

Quality: 652.00 Length: 228
 Ratio: 3.505 Gaps: 6
 Percent Similarity: 81.579 Percent Identity: 61.842

alignment_block:

us-09-805-550-4 x BI927022 ..
 Align seg 1/1 to: BI927022 from: 1 to: 771

```

1  MetLysLeuThrValIleThrsThrsLeuLysGlyThrsHisPheGluIleArgVa 17
    |||||||
101  ATGAAGCTCACTGTAAAGACTCTCAAGGAAAGTCACTTGAATAATAGGT 150
    |||||||
17  lGlnProAsnAspThrIleMetAlaValLysLysAsnIleGluIleG 34
    |||||||
151  TCAGCATCTGTATAGATTATGCGAGTCAGCAAGAACATTTGAAGATGAC 200
    |||||||
34  lnglyLysAspSerThrsProThrpglyGlnGlnleuLeuIlePheAsnGly 50
    |||||||
201  AAGCAAAAGATTAATTACCCATGTGGGACAGCTGCTGATTCACAAATGT 250
    |||||||
51  LysValIleLysAspGlySerThrsLeuGlnLysAsnlyrsValasngluAs 67
    |||||||
251  AAAGTGTGCTGAAGATGAAGATCAATCTTGGAAAAACAATGCTCTGAGGA 300
    |||||||
67  pGlyPheLeuValIleMetleuSerlysglyLysThrsSerlySerThrs 84
    |||||||
301  TGGTTTCTTGTGTCATGCTTAGCAGACAGCAAAACTCTAGCTCAAGTG 350
    |||||||
84  lyThrsSerSerSerGlnHisSerAsnThrProAlaThr..ArgGlnAla 99
    |||||||
351  GGACAACTTCTGCTCAGCAGCAGCAGCACTGCCCAATCTCACTACACAA 400
    |||||||
100  ProProLeuGlnAlaProGlnGlnAlaProGlnProProValAlaProIle 116
    |||||
401  CTTGAAGTATTCGCCCATTCACAGGCCCAAAA..GATGTTGTCTGACG 447
    |||||
116  eThrsThrsSerGlnProGlnlyLeuProAlaGlnAlaProAsnThrHisA 133
    |||||
448  TTCGATGCTCGCGGCTGCTAGCTTCACGT.....GATGATTATA 488
    |||||
133  spAsnAlaAlaSerAsnleuSerGlyArgAsnValAspThrIleIle 149
    |||||
489  GTCAAGCTGCATCAAAATTAATTAGTTGCTGCCAATTAATCTGACCAACTATA 538
    |||||
150  AsnGlnleuMetGluMetGlyGlySerThrpaAspLysAspLysValG1 166
    |||||
539  CACCAACTTATGATGATGGTGGTGGCAGCTGGGACAAAGACAGATTAC 588
    |||||
166  nArgAlaLeuArgAlaAlaIleArgAsnAsnProGlnArgAlaValGluIle 183
    |||||
589  TCGTCACTTCGAGCTGCTTATTAACAATCTGAAGAGCTGTGATTACT 638
    |||||
183  eutySerGlyIleProValThrAlaGluIleAlaValProIle.GlyG1 199
    |||||
639  TATATTCAGGAATTCCTGAACGGCAGAGATTCTGTATCGGTAAGCCG 688
    |||||
199  yGlnGlyAlaAsnThrThrsAspArgAlaProThrGlyGlu.....Alag 214
    |||||
689  GGGTGCATTAATCTGCT...GCTGTGCTACACCTGCGCTATTGAC 735
    |||||
214  lyLeuSerGlyIleProAsnThrAlaProLeu 224
    |||||
736  CTTCTTTCGGCAGCACTAATCTGCTCCCTTA 767

```

seq_name: gb_est1:AV912395

seq_documentation_block:

LOCUS	AV912395	614 bp	mRNA	linear	EST 18-JAN-2002
DEFINITION	AV912395 K. Sato unpublished cDNA library, cv. Akashinriki				
ACCESSION	AV912395				
VERSION	AV912395				
KEYWORDS	vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone				
SOURCE	Hordeum vulgare subsp. vulgare.				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.				
REFERENCE	Sato, K., Saitoh, D. and Takeda, K.				
AUTHORS	Barley EST sequencing project in NIG and Okayama Univ				
TITLE	Unpublished (2002)				
JOURNAL	Contact: Tadasu Shin-1				
COMMENT	National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshin@genes.nig.ac.jp.				
FEATURES	Location/Qualifiers				
source	1..614				
	/organism="Hordeum vulgare subsp. vulgare"				
	/cultivar="Akashinriki"				
	/db_xref="taxon:112509"				
	/clone="bak3m04"				
	/clone_lib="K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves"				
	/tissue_type="leaves"				
	/dev_stage="vegetative stage"				
	152 c 119 g 177 t 3 others				
BASE COUNT	163 a 152 c 119 g 177 t 3 others				
ORIGIN					
alignment_scores:					
Quality:	637.00	Length:	143		
Ratio:	4.684	Gaps:	0		
Percent similarity:	95.105	Percent identity:	84.615		
alignment_block:					
US-09-805-550-4 x AV912395/rev	..				
Align seg 1/1 to reverse of: AV912395 from: 1 to: 614.					
226	LeupheProGInG1YAlaSerAsnAlaG1YGLYAlaG1YGLYPr	242			
613	CTTTTCCCGCAGGGGCTTCCATGCTGGAGGTCGCTGGTGATG	564			
242	OleuAspPheLeuAArgAsnAsnProGInPheGInAlaValAArgGluMetY	259			
563	ACTGATTTTCTTCGAAATTAACCAACAGTTTCAGACACTTCGGAAATG	514			
259	AlHisThrAsnProGInnIleLeuGInPrometLeuValGluLeuSerLys	275			
513	TTCATATCAAAATCCACAAATTTTACAGCMTATCTCCACGAAATTTGAGCAAG	464			
276	GInAsnProGInnIleLeuArgLeuIleGluGluAsnHisAspGluPhe	292			
463	CAGATCCCACTCTTAAGTTGATTCAGGAGAACAAATGATGAGTTCCT	414			
292	uGInLeuLeuAsnGluProPheGluGluYGLYGLYAspPheLeuAspG	309			
413	TCAGTACTAATTAAGACATTTGAAGCGCGGAGTGGGACCTTTAGACC	364			
309	InProGluGluAspGluMetProHisAlaIleSerValThrProGluGlu	325			
363	AGCGTACCAACGATGGAATGCTCATGCTATCAAGTGTGACACAGAAAG	314			
326	GInGluAlaIleG1YArgLeuGluSerMetG1YpPheAspArgAlaArgA	342			

```

313 CAAGAGCGCAATTGGAAGGTTGGAAGCCATGCGGCTTTGACAGACGACAGCTGT 264
342 111eGua1aPheLeuAlaCysAspArgAsnGluGluLeuAlaAlaAsnT 359
|||||.....:|||||
263 CATCGAAGCATCTTTCGCTGTGACAGAGATGAGCAACTGCTGCAAACT 214
359 yfLeuLeuGluHsAlaGlyGluAsp 368
|||||.....:|||||
213 ATCTTTTGACGATGCTGTGTGACGAAGAA 185
seq_name: gb_est2:BE510591

seq_documentation_block:
LOCUS BE510591 365 bp mRNA linear EST 07-AUG-2000
DEFINITION 946054A04.x1 946 - tassal primordium prepared by Schmidt lab Zea
mays CDNA, mRNA sequence.
ACCESSION BE510591
VERSION BE510591.1 GI:9731839
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade: Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 365)
REFERENCE Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946054 row: A column: 04.
FEATURES
Source
Location/Qualifiers
1..365
/orrganism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/cclone_lib="946 - tassal primordium prepared by Schmidt
lab."
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="X10LR"
/note="Organ: tassels; Vector: HybriZAP; Site_1: EORI;
Site_2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."
94 a 99 c 77 g 95 t

BASE COUNT
ORIGIN
alignment_scores:
Quality: 633.00 Length: 121
Ratio: 5.231 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-805-550-4 x BE510591/rev ..

Align seg 1/1 to reverse of: BE510591 from: 1 to: 365

223 ProLeuAspLeuPheProGlnGlyAlaSerAsnAlaGlyGlyAlaG1 239
|||||.....:|||||
363 CCACATGATCTTTTCCCGCAGGGGCTTCCAAATGCTGAGAGTGCTGCTG 314
239 yGlyGlyProLeuAspPheLeuArgAsnAsnProGlnPheGlnAlaValA 256
|||||.....:|||||

```



```

seq_name: gb_est1:BE035647
seq_documentation_block:
LOCUS BE035647 967 bp mRNA linear EST 07-JUN-2000
DEFINITION MO13A05 M0 Mesembryanthemum crystallinum cDNA 5' similar to rad23,
mRNA sequence.
ACCESSION BE035647
VERSION BE035647.1 GI:8330656
KEYWORDS EST.
SOURCE common ice plant.
ORGANISM Mesembryanthemum crystallinum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
1 (bases 1 to 967)
Böhner,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferree
H., Kawasaki,S., Mccollough,A., Michalowski,C.B., Palacio,C.,
Scara,G., Wheeler,M. and Zeveda,G.R.
Functional genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski,C.B.
University of Arizona
Bio Sciences Dept room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
An open reading frame exists.
Insert Length: 1 Std Error: 0.00.
location/Qualifiers
1..967
/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone_id="MO"
/tissue_type="apical meristem and leaf primordia"
/dev_stage="5 weeks"
/note="no stress"
BASE COUNT 243 a 225 c 235 g 248 t 16 others
ORIGIN
alignment_scores:
Quality: 626.50 Length: 228
Ratio: 3.442 Gaps: 5
Percent Similarity: 79.825 Percent Identity: 57.456
alignment_block:
US-09-805-550-4 x BE035647 ..
Align seg 1/1 to: BE035647 from: 1 to: 967
151 GlnUmeGluMeGlyGlySerTPAsPlyAsPlyValGlnAr 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||
9 CAGATTCTTGATATGGGTGAGGAAAGCTGGACAGGACACGGTTGTCG 58
167 gAlaLeuArGAlaAlaATyrAsnAsnProGluArGAlaValGluTyrLeuT 184
|||||:|||||:|||||:|||||:|||||:|||||:|||||
59 ACCTTACGTGCAGCTTCACACACCTGAAGGGGTGTAAGATATTGTC 108
184 yTserGlyIleProValInThrAlaGluIle..... 193
|||||:|||||:|||||:|||||:|||||:|||||:|||||
109 ATTCTGGAAATTCCTGAGCAAGCTGAAGTCCCTCTGTCGAGCGCCT 158
194 ...AlaValProIleGlyGlyGlnGlyAlaAsnThrThrAspArGAlaPr 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||
159 GCTGCTGCTCTCGGGGTGGGAGGCTGCAAAATCCTTGGACAGGCTCC 208
209 O.....ThrGlyGluAlaGlyLeuSerGlyIleProA 220
|||||:|||||:|||||:|||||:|||||:|||||:|||||
209 TCAAGAGAGCTGCACATCGACAGGTCCAGCTCTACCAACAGCAGGTCTTA 258
220 snThrAlaProLeuAspIleuPheProGlnGlyAlaSerAsnAlaGly... 235

```

seq_name: gb_est1:AW508593

seq_documentation_block:

LOCUS AW508593 689 bp mRNA linear EST 03-DEC-2001
DEFINITION s144a09.y1 Gm-tr1030 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: ,
Gm-tr1030-785 5' similar to TR:003990 003990 RAD23, ISOFORM I. ; ,
mRNA sequence.
ACCESSION AW508593
VERSION AW508593.1 GI:7146671
KEYWORDS EST.

SOURCE soybean.
ORGANISM glycine max
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 689)
AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khana
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Stepien,M., Theising,D., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Page,B., Harvey,N., Schurk
,R., Ralter,E., Kohn,S., Shin,T., Jackson,I., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel.: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cculeresgen.com.
Insert Length: 975 Std Error: 0.00
High quality sequence stop: 440.
location/Qualifiers


```

source
1. .689
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-r1030-785"
/clone_lib="Gm-r1030"
/lab_host="DH10B"
/notes="vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
cDNA library was constructed from mRNA isolated from
immature cotyledons of greenhouse grown plants
(individual seed fresh weight of 100-300mg). The library
was prepared using the Life Technologies pSuperscript cDNA
library construction kit. Complementary DNA was
synthesized from mRNA using a poly(dT) sequence with a
NotI restriction site. SalI linkers adapters were ligated
to the blunt-ended cDNA fragments followed by NotI
digestion. The cDNA fragments were directionally cloned
into the NotI-SalI restriction site of the pSPORT1
vector. The ligated cDNA fragments were transformed into
E. coli Electromax DH10B host cells. This library was
constructed by Dr. Lila Vodka and Dr. Anu Khanna. Note
that Gm-r1030 is a re-track of Gm-cl007."

BASE COUNT      175 a      168 c      169 g      177 t
ORIGIN

alignment_scores:
Quality: 612.50      Length: 228
Ratio: 3.422      Gaps: 4
Percent Similarity: 78.509      Percent Identity: 58.772

alignment_block:
US-09-805-550-4 x AM508593 ..

Align seg 1/1 to: AM508593 from: 1 to: 689

136 AlaSerAsnLeuSerGlyArgAsnValAspThrIleIleAsnGlnLeu 152
|||||
1 GCATCTATATCTTGTGCTGGAAGTAACTTGAGGAGCAACATTCGCAAT 50
|||||
152 uMetGluMetGlyGlySerTrpAspIleValAlaGlnArgAlaL 169
|||||
51 CCTTGACATGGGTGAGAGAGCTGCGACAGGAGACTGTTCTGCTC 100
|||||
169 euArGAlaAlaIATyrAsnAsnProGluArgAlaValGluTyrLeuTyrSer 185
|||||
101 TTGCTGCTGCTTATACACCTGAGAGAGCTGTGATATTGTATTC 150
|||||
186 GlyIleProValThrAlaGlu.....IleAlaValProIleG1 198
|||||
151 GGCATATCCAGACGACGAGCTCCACGCTGTTACCCGAGAGCTGCAAG 200
|||||
198 yGlyGlnGlyAlaAsnThrThrAspArgAlaProThrGlyGluAlaGlyL 215
|||||
201 TGCTCAACCTGCAAAATCCTCAGCTGCTGCCACAGCAGCAACACAG 250
|||||
215 eu.....SerGlyIleProAsnThrAlaProLeuAsnProLeuPro 228
|||||
229 GlnGlyAlaSerAsnAlaGly...GlyGlyAlaGlyGlyGlyProLeuAs 244
|||||
301 CAGGGCTTCCAAATGTTGGTCTGCTGCTGCTGCTGCTGCTTTAGA 350
|||||
244 pPheLeuArgAsnAsnProGlnPheGlnAlaValArgGluMetValHisT 261
|||||
351 CTTTCTTCGACACAGTCACAGCTTCCAGGCTTACGGCATATGTTACAG 400
|||||
261 hTrsAsnProGlnIleLeuGlnProMetLeuValGluLeuSerTyrGlnAsn 277
|||||
401 CTATATCCAAATATTTGACCTATGCTACAGAGCTTGGCAACAAAT 450
|||||
278 ProGlnIleLeuArgLeuIleGluGluAsnHisAspGluPheLeuGlnLe 294
|||||

```

```

451 CCTCATCTTATGCGATTGATTCAGAGCATCACTGTGACTCTTCGCT 500
294 uLeuAsnGluProPheGluGlyGlyGluGlyAspPheLeuAspGlnPro 311
|||||
501 AATTAATGAACCCGTGTGAGGGGTGAGGGAATATATCTGGGACAG...C 547
|||||
311 lUGluAspGluMetProHisAlaIleSerValThrProGluGluGlnL 327
|||||
548 TAGCTAGTGCATCCCGACAGCACTGACAGTACACCCCTGAGGAAG. CAA 596
|||||
328 AlalleGlyArgLeuGluSerMetGlyPheAspArgAlaArgValIleG1 344
|||||
597 GCAATGTGACGCTCTCGAAGCAATGGGAGTATGCTGCACTGTAATTGA 646
|||||
344 uAlaPheLeuAlaCysAspArgAsnGluGluLeu 355
|||||
647 GGTGTACTCTGCTGTGTTACAAATGAGGAGACTG 680
|||||

```

seq_name: gb_est2:BG445098

seq_documentation_block:

LOCUS BG445098 899 bp mRNA linear EST 15-MAR-2001
DEFINITION GA_Ea0026M08f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0026M08f, mRNA sequence.

ACCESSION BG445098
VERSION BG445098.1 GI:13354750

KEYWORDS EST.

SOURCE Gossypium arboreum.

ORGANISM Gossypium arboreum.

REFERENCE Wing,R.A., Frisch,D., Yu,Y., Maln,D., Rambo,T., Simmons,J., Henry

AUTHORS D., Wood,T.C., Leslie,A. and Wilkins,T.A.

TITLE An integrated analysis of the genetics, development, and evolution

JOURNAL of the cotton fiber

COMMENT Unpublished (2000)

Contact: Wing RA

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: TATACGACTCACTATAGG

High quality sequence stop: 772.

Location/Qualifiers

1. .899

/organism="Gossypium arboreum"

/strain="AKA"

/cultivar="8400"

/db_xref="taxon:29729"

/clone="GA_Ea0026M08f"

/clone_lib="Gossypium arboreum 7-10 dpa fiber library"

/tissue_type="fibers isolated from bolls harvested 7-10

dpa"

/lab_host="E. coli"

/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

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BASE COUNT      256 a      206 c      215 g      221 t
ORIGIN

alignment_scores:
Quality: 612.00      Length: 301
Ratio: 2.873      Gaps: 9
Percent Similarity: 70.764      Percent Identity: 46.844

alignment_block:
US-09-805-550-4 x BG445098 ..

Align seg 1/1 to: BG445098 from: 1 to: 899

```

```

26 VAllyLysAsnIleGluGluIleGlnGlyLysAspSerTyrrProtrpG1 42
   |||||
10 GTAAAAAGAACATAGAAACGTTCACAGGAGCTGTTATTCCTGCTTC 59
   |||||
42 yGlnGlnLeuLeuIlePheAsnGlyLysValLeuLysAspGluSerThL 59
   |||||
60 ACAACAAATGCTATATCTATAGGAAAAAGTTCTTAAAGATGACAGCAC 109
   |||||
59 euGluGluAsnLysValAsnGluAspGlyPheLeuValValMetLeuSer 75
   |||||
110 TGGCTGAAAAACAGTGTCTACGAAATAGCTTATCTGATCATGTTAA 159
   |||||
76 LysGlyLysThrSerGlySerThrGlyThrSerSerSerGlnHisSerS 92
   |||||
160 AAGAAATTAAG.....GGTACAACTGGTGAGGGTTCACCT.....GCTTC 197
   |||||
92 nThrProAlaThrArgGlnAlaProProLeuGluAlaProGlnGlnAla 109
   |||||
198 AACAGCTCCTACAAAGAAAGCTCTGAGGCAAGTATCTGCCAACAGCTC 247
   |||||
109 roGlnPro...ProValAlaProIleThrThrSerGln..... 120
   |||||
248 CAGCACACAGCTTCTACTGCACCTGTTCACACGCTATGCTGCACGCT 297
   |||||
121 .....ProGluGlyLeuProAlaGlnAlaProAs 130
   |||||
298 GCCACTGAATGCTGCTGCTGCTTCAAGTACTCTTCTCAGATTCCTGA 347
   |||||
130 nThrHisAspAsnAlaAlaSerAsnLeuLeuSerGlyArgAsnValAsp 147
   |||||
348 TGTATTATGGCCAAAGCAGCATCTAACCTGGTTGCGAGGATACCTAGAG 397
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147 hTleIleAsnGlnLeuMetGluMetGlyGlyGlySerTrpAspLysasp 163
   |||||
398 GAACAATCCAAACAGATCTGTGATATGCGGAGGAGCACTGGGAGAGGAC 447
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164 LysValGlnArgAlaLeuArgAlaAlaIleArgAsnAsnProGlnAla 180
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448 ACTGTGTGCCACGCCCTTGCTGCTCTTATATTAATTAACCCAGAGAGCT 497
   |||||
180 LgluTyrrLeuTyrrSerGlyIleProValThrAlaGlu.....I 193
   |||||
498 TGAATATTGTTATCTGGCATCCCGAGCAAGCTGAGGTCACCTGCG 547
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193 LeAlaValProIleGlyGlnGlyAlaAsnThrThrAspArg..... 207
   |||||
548 CCCGTGCTCTGTAGTGGCCAAACCAACTGCTGCACAACTCTCA 597
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208 .....AlaProThrGlyGlnAlaGlyLeuSerGlyIleProAsnThrAl 222
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598 CAGCGTCGACAAACGGCAGCTATTCCTGCACAGTGA...CCAAATGCA 644
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222 aProLeuAspLeuPheProGlnGlyAlaSerAsnAlaGly...GlyGly 238
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645 TGCATTAGACCTCTTCCCAAGGCTTCCCAACATGGGTGCAAGTGG 694
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238 laGlyGlyGlyProLeuAspPheLeuArgAsnAsnProGlnPheGlnAla 254
   |||||
695 CTGAGGCTGGCAGCTCTTGATTTTACGAAACAGTACAGATTCACACT 744
   |||||
255 ValArgGluMetValIleThrAsnProGlnIleLeuGlnPrometLeuVa 271
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745 TTGCGAGCAATGTCGCAAGCCATCCAAATATTGGAGGCCATCTTCA 794
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271 LgluLeuSerLysGlnAsnProGlnIleLeuArgLeuIleGluGluAsn 287
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795 AGGAGTGGGGAANCAAAATGCTATTTATGAAACTATACAGAGAGCT 844
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288 HisAspGluPheLeuGlnLeuLeuAsnGluProPheGluGlyGlyGlu 304
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845 CAGGCTGATTTCTTCTGATCAAGAACCTGCGTGAAGTGGAGG 894
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304 y 304

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seq_name: gb_est2:BG585286
895 A 895
seq_documentation_block:
LOCUS BG585286 817 bp mRNA linear EST 11-APR-2001
DEFINITION EST487049 MHAM Medicago truncatula/Glommus versiforme mixed EST
ACCESSION library cDNA clone pMHAM-22M22 5' end, mRNA sequence.
VERSION BG585286
KEYWORDS BG585286.1 GI:13600350
SOURCE Medicago truncatula/Glommus versiforme mixed EST library.
ORGANISM Medicago truncatula/Glommus versiforme mixed EST library
Eukaryota; mixed EST libraries.
REFERENCE Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.
AUTHORS 1 (bases 1 to 817)
TITLE ESTs from roots of Medicago truncatula after colonization with
Glommus versiforme, 2001
JOURNAL Unpublished (2001)
COMMENT Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N380759e TIGR sequence name: MFDGB83mk More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gaa cta gac gat cc).
FEATURES
Location/Qualifiers
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/organism="Medicago truncatula/Glommus versiforme mixed EST
library"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pMHAM-22M22"
/clone_id="MHAM"
/tissue_type="roots colonized with Glommus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glommus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XL0LR"
/note="Vector: pBluescript SK-. Site.1: EcoRI; Site.2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glommus versiforme. The cDNA was
directionally ligated into the UniZap XR vector from
stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0LR cells."
BASE COUNT 229 a 217 c 178 g 193 t
ORIGIN
alignment_scores:
Quality: 604.50 Length: 283
Ratio: 2.906 Gaps: 9
Percent Similarity: 73.498 Percent Identity: 49.470
alignment_block:
US-09-805-550-4 x BG585286 ..
Align seg 1/1 to: BG585286 from: 1 to: 817
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7 GTTCTGAGAAATAGTTTATCTGATCATGTTGCCAAGATTAAGCTATC 56
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79 .ThSerGlySerThrGlyThrSerSerSerGlnHisSerAsnThrProA 95
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```

```

57 ATGACGTGAGCCCTGCTGCTCAGCTGCCGCCACGGCAGCTCCACACTG 106
95 laThrArgGlnAlaProProLeuGlnAlaProGlnGlnAlaProGlnPro 111
107 CAAGTCTTGGCTCTCTTGTTCACACCTCAG..... 141
112 ProValAlaProLeuThrThrSerGlnProGlnGlnLeuProAlaGln.. 127
142 CCGTCTCTCTCA...ACTGTCGACAGGAGAAATCCAAATCTGCGCAGAG 188
128 .....AlaProAsnThrHisAspAsnAlaAlaSerAsnLeuAsn 141
189 TCCGTTGTTACTCTCTCCACTACTGTGCGCCGAACTCTATCTCATGTG 238
141 erGlyArgAsnValAspThrThrIleIleAsnGlnLeuMetGlyGly 157
239 CTGGAAACACTTTTAGAACCAACTATTCACAAATTCAGAAATGGGGGA 288
158 GlySerTrpAspLysAspLysValGlnArgAlaLeuArgAlaAlaTyrAs 174
289 GGAAGTTGGGATCGGACACTGTGATCCGAGCTCTGCTGCTCATATAA 338
174 naaProGlnArgAlaValAlaGluTyrLeuTyrSerGlyIleProValThr 191
339 CAATCCCGAAAGAGCGGTGATATCTATATCTGCGATGCCGACACAG 388
191 laGlu.....IleAlaValProIleGly...GlyGlnGlyAlaAsn 203
389 CTGAAGCTCCAGACGAGTGTGCATCCACCAATGTGGGACGCGAAGAAC 438
204 ThrThrAspArgAlaProThrGlyGlnAlaGlyLeuSerGlyIleProAs 220
439 CCTTCACCCAGGCTCCAGCCCAACTAGCTGTGCTGTGGGCCCAA 488
220 nThrAlaProLeuAspLeuPheProGlnGlyAlaSerAsnIleGlyGly 237
489 CACCAACCCACTATACCTTGTCTCCCTCAGGCGCATCCCAATTTGGGTG 538
237 LysAlaGlyGlyGlyProLeuAspPheLeuArgAsnAsnProGlnPheGln 253
539 ATGAAATGCGAGTGTGGAATTCCTGCGAACAACAGTCACAGTTCCAA 588
254 AlaValArgGluMetValHisThrAsnProGlnIleLeuGlnPrometLe 270
589 GCCTTGGAACAATGTGCAAGCAACCCCTCAATCTTACAGCCATGCT 638
270 uValGluLeuSerLysGlnAsnProGlnIleLeuArgLeuIleGluGlu 287
639 TCAGGAACCTAGGAAACAAATCCAAACCTATATGGAACCTATCCAGAGC 688
287 snHisAspGluPheLeuGlnLeuLeuAsnGlnProPheGlnGlyGly 303
689 ATCAAGCTGACTTCTTACGCTCTTATAATGAGCCT.....GGAGGCGAA 732
304 GlyAspPheLeuAspGlnProGlnGlnAspGluMet.....Pr 316
733 GAGAACCTA.....GAGGAGACATTAAGTGTGCTTGGCTCC 767
316 ohHisAlaIleSerValThrProGlnGlnGlnAlaIleGlyArgLeu 332
768 TCAGACCATTACTATACACCCAGAAAGAGAACGAGCCATTCACAGGCTT 816

seq_name: gb_est2:BI973998

seq documentation block:
LOCUS BI973998 592 bp mRNA linear EST 30-NOV-2001
DEFINITION sal15d11.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1065-8637 5' similar to TR:003991 003991 RAD23 PROTEIN,
ISOFORM II, mRNA sequence.
ACCESSION BI973998
VERSION BI973998.1 GI:16348403
KEYWORDS EST.
SOURCE soybean.

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```

ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 592)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,
A., Bolla,B., Matra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,
R., Riller,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,
R., Waterston,R. and Wilson,R.
Public Soybean EST Project
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800) 533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
Location/Qualifiers
FEATURES
source
1..592
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1065-8637"
/tissue_type="germinating shoots"
/lab_host="DH10B"
/note="Vector: PBscript II SK-; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
germinating shoots of the cultivar Williams. The seeds
were allowed to germinate for 24 hours prior to being
cold stressed for 2 days at 4C. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(AT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."
BASE COUNT 176 a 125 c 128 g 163 t
ORIGIN
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Quality: 602.50 Length: 197
Ratio: 3.742 Gaps: 2
Percent Similarity: 81.726 Percent Identity: 60.914
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US-09-805-550-4 x BI973998 ..
Align seg 1/1 to: BI973998 from: 1 to: 592
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2 AAGACTTTGAAAGGAGGACCATTCGAAATTCAGAGGTTCACACCTCGATAC 51
22 rIleMetAlaValLysLysAsnIleGlnGlnIleGlnLysAspSer 39
|||||
52 TGTATGTGCTGTCAAGAAATATTGAAGATGTACAAAGAAAGATTAATT 101
39 yPProTrpGlyGlnGlnLeuLeuIlePheAsnGlyLysValLeuLysAsp 55
|||||
102 ACCCATGTGCACAGCAATTTGATTTCACAAATGCGAAGCTTTGAAAGAT 151

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56  G1uSerThrLeuGluGlnAsnLysValAsnGluAspGlyPheLeuVala 72
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152  GAACACGACTTAGTAGAGATAAGCTCTGAAAGAGCGCTTCTGTGT 201
72  MetLeuSerLysGlyValThrSerGlySerThrGlyThrSerSerSerg 89
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
202  TATGCTTAAAGATAAGATACATCAGGTGTGCTGCAGCTGCTGCTT 251
89  LnhISerAsnThrProAlaThr.....ArgGlnAlaPro 100
||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
252  AAGCTGACGATATCTCTACGACTGATCAACGTCAATTCACCCGT 301
101  ProLeuGluAlaProGlnGlnAlaProGlnProProValAlaProIle 117
||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
302  CCTTCGATCCCTCAGTGCAACTCAAGCTGCACACACAGTACATCTAG 351
117  rThrSerGlnProGluGlyLeuProAlaGlnAlaProAsnThrHisAsp 134
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352  CACAGATGCCCA.....ACTACAAATGTGCTGCAGATACCTTAGCTC 395
134  snAlaAlaSerAsnLeuLeuSerGlyArgAsnValAspThrIleIleAsn 150
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396  TGGCTGCTCGAATTTAGTGTGGTAGTAATCTTGACGACGACTATCA 445
151  GlnLeuMetGluMetGlyGlyGlySerThrPaspLysAspLysValGln 167
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446  CAATTTATGGACATGGGTGGCATTTGGGACAGACACAGATTGTGTG 495
167  gAlaLeuArgAlaAlaTyrAsnAsnProGluArgAlaValGluTyrLeu 184
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
496  TCGCTCTCAGCAGCTTATATATACCCACAGCGCTGATAGATTACTTGT 545
184  ySerGlyIleProValThrAlaGluIleAlaValProIle 197
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seq_name: gb_est2:BM113219

seq_documentation_block:
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DEFINITION EST560755 potato roots Solanum tuberosum cDNA clone cPRO17N13 5'
end, mRNA sequence.
ACCESSION  BM113219
VERSION    BM113219.1  GI:17076267
KEYWORDS   EST.
SOURCE     potato.
ORGANISM   Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
            1 (bases 1 to 691)
            van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
            Uiterback,T., Chienlung,A., Bougri,O., Buell,C.R., Ronning,C.,
            Tanksley,S. and Baker,B.
            Generation of ESTs from potato roots
            Unpublished (2001)
            Contact: Research Genetics, Libraries Division
            Tel: 1-800-711-6195
            Email: cdna@resgen.com
            For clone info: please contact Research Genetics, Libraries
            Division tel 1-800-711-6195, email cdna@resgen.com
            Seq primer: 13.

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                /clone_id="potato roots"
                /tissue_type="roots"
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                /lab_host="SOLR"
                /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

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XhoI; supplier: Cornell University, Tanksley lab;
sequencing; The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."

BASE COUNT      182 a      158 c      163 g      188 t
ORIGIN

alignment_scores:
    Quality: 593.50      Length: 200
    Ratio: 3.619      Gaps: 4
    Percent Similarity: 82.000      Percent Identity: 61.500

alignment_block:
us-09-805-550-4 x BM113219 ..
Align seg 1/1 to: BM113219 from: 1 to: 691

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1  GCTGATATTAACAATCCAGAAAGAGCTATGATATCTGATCTGTAT 50
187  eProValThrAlaGluIle.....AlaValProIleGlyGlyGlnGly 202
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51  TCCTGAGCAAGCAAGAAATCCACACTGCTGCTGCCAGCGGACAGCTG 100
202  LAsnThrThrAspArgAlaProThrGlyGluAlaGlyLeuSerGlyIle 218
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101  TAAATCTCCAGTTCAGGCT...TCACAGCCAGCAGTTCGCTCCGTGG 147
219  ProAsnThrAlaProLeuAspLeuPheProGlnGlyAlaSerAsnAla 235
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148  CCNAATGCTATATCTTGGATCTCTTCCCTCAGGCGCTTCCAAATGTGG 197
235  yGlyGlyAlaGlyGlyGlyProLeuAspPheLeuArgAsnAsnProGln 252
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
198  TTCAAATGTTGGAGCTGGAATTTGGATTGTTCAACCAATAGTCCACAG 247
252  heGlnAlaValArgGluMetValHisThrAsnProGlnIleLeuGlnPro 268
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
248  TTCACGCCCTCCGACGAAATGCTCAAGCAACCCACAGATATTGCGACCA 297
269  MetLeuValGluLeuSerLysGlnAsnProGlnIleLeuArgLeuIle 285
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
298  ATGCTCCAGAGATGGGTGAAGCAAAATCCTCAATGTATGGGCTGATCA 347
285  uGluAsnHisAspGluPheLeuGlnIleLeuAsnGluProPheGluGly 302
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
348  AGAGCATCAAGCTGACTTCTGGCCCTCATCAATGTGAACCGTTGAG... 394
302  LyGluLysAspPheLeuAspGlnProGluGluAspGluMetProHisAla 318
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395  GGGAAAGGAACGCTCCCTGGGCGACCG...GCAAGGCGCTATACCAACA 441
319  LLeSerValThrProGluGlnGlnAlaIleGlyArgLeuGluSerHe 335
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
442  GTGACTGTCACACCTGAAGCGGTGAGGCTATGAGCACTTGAACCTAT 491
335  tGlyPheAspArgAlaArgValIleGlnAlaPheLeuAlaCysAspArg 352
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492  GGGTTTTCGATCGAGCTTGGTGGCAAGTATTTTGGATGCAACAAAA 541
352  snGluLysLeuAlaAlaAsnTyrLeuLeuGlnHisAlaGlyGluGln 368
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
542  ATGAGAGATGGCTGCAAACTATCTGTAGATCAATGCATGAGTTGAT 591

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